AMENDMENT TO THE SPECIFICATION

Please replace the paragraph beginning at page 4, line 23 with the following amended paragraph.

As one of ordinary skill in the art would recognize, the above-described method can be practiced with a variety of GPCR-like receptors. For example, the GPCR-like receptor used in the screening method may be encoded by a polynucleotide having a sequence set forth in any one of SEQ ID NOS:43, 21, 45, 35, 7, 106, and 104. As noted above, such GPCR-like receptors may be used in screening assays designed to measure a GPCR-like receptor activity, including binding activity. Expressly contemplated are embodiments of the screening method comprising a GPCR-like receptor encoded by a polynucleotide comprising a sequence set forth in SEQ ID NO:43 and a peptide comprising a sequence selected from the group consisting of SEQ ID NOS:85, 86, 88, 89, and 118, wherein the peptide binds to the GPCR-like receptor. More particularly, a screening method wherein the GPCR-like receptor is encoded by a polynucleotide having the sequence set forth in SEQ ID NO:43 is provided. In an alternative embodiment, the GPCR-like receptor comprises a sequence set forth in SEQ ID NO:21 and the peptide comprises a sequence selected from the group consisting of SEQ ID NOS:78, 79, 80, 84, 87, 92, 98, 100, 120, 171, 143, 122, 123, 97, 85, 83, 101, 102, 93, 88, 91, 94, 93, 90, 152, 153, 154, 155, 156, 157, 80, 158, 119, 159, 160, 161, 162, 163 and 164. Another embodiment involves a GPCR-like receptor comprising a sequence set forth in SEQ ID NO:45 and a peptide comprising a sequence selected from the group consisting of SEQ ID NOS:86, 118, 125, 88, 126, 127, 128, 129, 102, 131, 100, 133, 92, 135, 136, 137, 87, 139, 91, 141 and 83. In yet another embodiment, the GPCR-like receptor comprises a sequence set forth in SEQ ID NO:35 and a peptide comprising a sequence selected from the group consisting of SEQ ID NOS:99, 97, 96, 77, 82, 81, 87, 100, 92, 80, 98, 120, 121, 79 and 84. In still another embodiment, the GPCR-like receptor comprises a sequence set forth in SEQ ID NO:7 and a peptide comprising a sequence selected from the group consisting of SEQ ID NOS:94, 103, 95, 101, 85, 79, 84, 87, 86, 80, 92, 100, and 180. Yet another embodiment involves a GPCR-like receptor comprising a

sequence selected from the group consisting of SEQ ID NO:106 and a peptide comprising a sequence selected from the group consisting of SEQ ID NOS:80, 92, 98, 100, 120, 121, 79, 84, 136, 87 and 86. Still another one of the many embodiments of this aspect of the invention involves a GPCR-like receptor comprising a sequence set forth in SEQ ID NO:104 and a peptide comprising a sequence selected from the group consisting of SEQ ID NOS:80, 92, 98, 100, 120, 121, 79, 84, 136, 87, 86, 150, 151, 133, 165, 91, 166, 131 and 167.

Please replace the paragraph beginning at page 10, line 6 with the following amended paragraph.

The invention also provides an isolated polynucleotide encoding a GPCR-like receptor. Such polynucleotides may be selected from the group consisting of: (a) a polynucleotide comprising a nucleotide sequence encoding any one of the amino acid sequences set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 105, 107, 109, 111, 113, 115 117, 177, and 179 (including the nucleotide sequences set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 104, 106, 108, 110, 112, 114, 116, 176, and 178); and (b) a polynucleotide which hybridizes under conditions of high stringency to the complement of the polynucleotide of (a). Exemplary conditions of high stringency are provided below. Such polynucleotides also include polynucleotides that exhibit at least 90%, at least 95%, at least 98%, at least 99% or at least 99.9% sequence identity to either a polynucleotide sequence disclosed in the sequence listing (*i.e.*, SEQ ID NOS: 1, 3, 5, 7, 9, 11, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 104, 106, 108, 110, 112, 114, 116, 176 and 178) or to a polynucleotide encoding a GPCR-like receptor comprising one of the sequences disclosed in the sequence listing (*i.e.*, SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 105, 107, 109, 111, 113, 115, 117, 177, and 179). Any one of the publicly available algorithms (*e.g.*, the BLASTl program of GCG) for comparing sequences may be used in determining the degree of sequence similarity (including appropriate penalties for gap

introductions). A preferred algorithm is the BLAST algorithm implemented at the GenBank website under the auspices of the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/BLAST/)~~ using default parameters. A polynucleotide of the invention may be partially or wholly chemically synthesized and embraces an anti-sense polynucleotide which specifically hybridizes to the complement of one or more of the above-described polynucleotides. In related aspects, the invention comprehends vectors comprising these polynucleotides preferably operably linked to expression control sequences, including expression vectors, as well as non-native host cells transformed or transfected with a polynucleotide in accordance with the invention or a host cell transformed or transfected with a vector of the invention. All suitable native and non-native host cells are embraced by the invention, including mammalian cells (*e.g.*, COS cells, CHO cells, HEK293 cells), insect cells (*e.g.*, *Drosophila melanogaster* S2 cells, *Spodoptera frugiperda* Sf9 cells, High-5 cells), yeast cells, bacterial cells (e.g., *E. coli*) and helminthic cells. The suitability of a particular cell for use as a host cell in accordance with the invention will depend on the ability to introduce a polynucleotide of the invention into the cell by any known means of transformation or transfection. Preferred host cells will also be capable of stably maintaining the introduced polynucleotide and will present a minimum of obstacles to propagation.

Please substitute Table 5 as provided below for original Table 5 beginning on page 24, line 1.

Table 5
***C. elegans* FMRFamide-related peptides (FaRPs) and encoding genes**

GENE AND CHROMOSOME NUMBER	STRUCTURALLY CHARACTERIZED FaRPs	SEQ ID NO:	PEPTIDES PREDICTED FROM GENE	SEQ ID NO:
FLP-1	SDPNFLRFa SADPNFLRFa SQPNFLRFa ASGDPNFLRFa AAADPNFLRFa	181 182 183 184 185	KPNFMRYa AGSDPNFLRFa SQPNFLRFa ASGDPNFLRFa SDPNFLRFa AAADPNFLRFa SADPNFLRFa KPNFLRFa	186 187 183 184 181 185 182 188
FLP-2			LRGEPIRFa SPREPIRFa	189 190
FLP-3			SPLGTMRFa TPLGTMRFa SAEPFGTMRFa NPENDTPFGTMRFa ASEDALFGTMRFa EDGNAPFGTMRFa EAEEPLGTMRFa SADDSAPFGTMRFa NPLGTMRFa	191 192 193 194 195 196 197 198 199
FLP-4			PTFIRFa ASPSFIRFa	200 201
FLP-5			APKPKFIRFa AGAKFIRFa GAKFIRFa	202 203 204
FLP-6	KSAYMRFa	205	(6 copies) KSAYMRFa	205
FLP-7			(2 copies) TPMQRSSMVRFa (3 copies) SPMQRSSMVRFa SPMERSAMVRFa SPMDRSKMVRFa	206 207 208 209
FLP-8			(3 copies) KNEFIRFa	210
FLP-9	KPSFVRFa	211	(2 copies) KPSFVRFa	211

FLP-10			QPKARSGYIRFa	212
FLP-11			AMRNALVRFa ASGGMRNALVRFa NGAPQPFVRFa	213 214 215
FLP-12			RNKFEFIRFa	216
FLP-13			SDRPTRAMDSPLIRFa (2 copies) AADGAPLIRFa (2 copies) APEASPFIRFa ASPSAPLIRFa SPSAVPLIRFa SAAAPLIRFa ASSAPLIRFa	217 218 219 220 221 222 223
FLP-14			(4 copies) KHEYLRFa	224
FLP-15			GGPQGPLRFa GPSGPLRFa	225 226
FLP-16			AQTFVRFa GQTFVRFa	227 228
FLP-17			(2 copies) KSAFVRFa KSQYIRFa	229 230
FLP-18			DFDGAMPGVLRFa DMPGVLRFa KSVPGVLRFa SVPGVLRFa EIPGVLRFa SEVPGVLRFa DVPGVLRFa SVPGVLRFa	231 232 233 234 235 236 237 238
OTHER PUTATIVE FLP GENES			TKFQDFLRFa AMRNSLVRFa DYDFVRFa DGFVRFa AFFKNVLRFa	239 240 241 242 243

"a" means amide.

Please replace the paragraph beginning at page 31, line 9 with the following amended paragraph.

The Wormpep database, containing all of the predicted protein sequences encoded by the *C. elegans* genome, used in these studies, was obtained through the Sanger Centre Web site ~~(http://www.sanger.ac.uk/Projects/C_elegans/)~~. Wormpep versions 13 (2/13/98) through 23 (released September 4, 2000). This database contains 19,430 protein sequences, including 388 splice variants. *C. elegans* genomic DNA sequences were accessed through ACEDB (Release WS3 4-25). The databases were searched and manipulated using programs from the Wisconsin Package GCG programs.

Please replace the paragraph beginning at page 73, line 19 with the following amended paragraph.

Based on analyses to date, the invertebrate GPCR-like receptors do not appear to have highly similar sequences in other organisms, such as vertebrates and plants. However, receptors bearing lower levels of similarity, *e.g.*, 55%, 60%, 65%, 70%, 75%, 80%, 85%, and preferably 90%, 95%, 98%, 99% and more preferably 99.5% similarity to a GPCR-like receptor amino acid sequence disclosed herein are also contemplated by the invention. Analogously, the invention comprehends receptor-encoding polynucleotides exhibiting 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, and preferably 95%, 98%, 99% and more preferably 99.5% similarity to a polynucleotide disclosed herein. Similarities can be determined using any of a variety of algorithms known in the art, with the BLAST algorithm implemented at the GenBank website ~~(http://www.ncbi.nlm.nih.gov/BLAST/)~~ under the auspices of the National Center for Biotechnology Information, using default parameters, being preferred. These receptor sequences are anticipated to be useful in a variety of contexts. For example, it is expected that vertebrate, and more particularly mammalian, receptor sequences showing some similarity to the invertebrate GPCR-like receptors will be useful in diagnosing, and treating, a variety of neurological ailments or conditions.

Please substitute Table 6 as provided below for original Table 6 beginning on page 34, line 9.

Table 6

~~SIN~~ Name	SEQ ID NO:	TM1		TM2		TM3		TM4		TM5		TM6		TM7	
		start	end	start	end	start	end	start	end	start	end	start	end	start	end
CEGPCR1a	1	47	71	83	109	121	142	161	181	213	233	262	282	298	321
CEGPCR1f	3	47	71	83	109	121	142	161	181	213	233	277	297	313	336
CEGPCR2	176	42	66	78	104	116	137	158	178	204	224	320	340	351	374
CEGPCR3	44	26	50	62	88	100	121	140	160	196	216	252	272	285	308
CEGPCR4	21	28	52	64	90	102	123	142	162	192	212	256	276	293	316
CEGPCR5	45	40	64	76	102	114	135	154	174	212	232	272	292	305	328
CEGPCR6	23	12	36	48	74	85	106	126	146	178	198	229	249	263	286
CEGPCR7	26	27	51	63	89	101	122	141	161	192	212	278	298	322	345
CEGPCR8	27	30	54	66	92	104	125	146	166	194	214	244	264	283	306
CEGPCR9	29	51	75	87	113	125	146	167	187	239	259	330	350	368	391
CEGPCR11	31	25	49	61	87	99	120	139	159	189	209	246	266	286	309
CEGPCR12c	5	38	62	74	100	112	133	157	177	207	227	255	275	291	314
CEGPCR12h	7	38	62	74	100	112	133	157	177	207	227	255	275	291	314
CEGPCR12u	9	38	62	74	100	112	133	157	177	207	227	255	275	291	314
CEGPCR12v	11	38	62	74	100	112	133	157	177	207	227	255	275	291	314
CEGPCR13	13	27	51	63	89	101	122	141	161	190	210	276	296	320	343
CEGPCR14	15	30	54	65	91	103	124	143	163	198	218	254	274	299	322
CEGPCR15	33	62	86	98	124	136	157	176	196	235	255	285	305	321	344
CEGPCR16	36	29	53	65	91	103	124	143	163	193	213	250	270	287	310
CEGPCR17	37	36	60	72	98	110	131	150	170	220	240	274	294	306	329
CEGPCR18a	17	10	34	46	72	84	105	126	146	185	205	282	302	320	343
CEGPCR19.1	106	56	80	92	118	130	151	170	190	228	248	287	307	324	347
CEGPCR19.2	104	56	80	92	118	130	151	170	190	228	248	287	307	324	347
CEGPCR20	41	44	68	79	105	117	138	159	179	215	235	283	303	323	346
CEGPCR21	108	76	100	112	138	151	172	193	213	249	269	336	356	373	396
CEGPCR22	110	55	79	95	121	132	153	173	193	233	253	279	299	319	342
CEGPCR23	112	21	45	64	90	101	122	142	162	203	223	249	269	287	310
CEGPCR24a	114	51	75	87	113	128	149	170	189	223	243	279	299	316	339
CEGPCR24b	116	51	75	87	113	128	149	170	189	223	243	279	299	316	339

~~Where "SIN" refers to SEQ ID NOS.~~